Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application.

1. (canceled).

2 (currently amended). ~~The~~ A method ~~of claim 1, wherein the~~ of assaying a *Brassica* plant for imidazolinone herbicide tolerance conferred by the PM1 mutation of the *B. napus AHAS1* gene, the method comprising the steps of:

a) isolating genomic DNA from the plant;

b) selectively amplifying an *AHAS1* gene from the genomic DNA using an *AHAS1* forward primer ~~has the~~ having a sequence as set forth in nucleotides 1 to 22 of SEQ ID NO:9 and an *AHAS1* reverse primer in a first amplification step, thereby producing an *AHAS1* reaction mixture;

c) removing the *AHAS1* primers from the *AHAS1* reaction mixture to produce a purified *AHAS1* reaction mixture;

d) in a second amplification step, further amplifying a portion of the amplified *AHAS1* gene containing the site of the PM1 mutation, by combining the purified *AHAS1* reaction mixture with a PM1 forward primer and a PM1 reverse primer, wherein the PM1 forward primer and the PM1 reverse primer bind to sites nested within the amplified portion of the *AHAS1* gene;

e) denaturing the product of the second amplification step to produce single stranded polynucleotides that are allowed to adopt unique conformations by intramolecular interactions; and

f) detecting the presence or absence of the PM1 mutation on the basis of the mobility of said single stranded polynucleotide conformers in a substrate.

3 (currently amended). ~~The~~ A method ~~of claim 1, wherein~~ of assaying a *Brassica* plant for imidazolinone herbicide tolerance conferred by the PM1 mutation of the *B. napus AHAS1* gene, the method comprising the steps of:

a) isolating genomic DNA from the plant;

b) selectively amplifying an *AHAS1* gene from the genomic DNA using an *AHAS1* forward primer and an *AHAS1* reverse primer ~~has the~~ having a sequence as set forth in nucleotides 1 to 22 of SEQ ID NO:10 in a first amplification step, thereby producing an *AHAS1* reaction mixture;

c) removing the *AHAS1* primers from the *AHAS1* reaction mixture to produce a purified *AHAS1* reaction mixture;

d) in a second amplification step, further amplifying a portion of the amplified *AHAS1* gene containing the site of the PM1 mutation, by combining the purified *AHAS1* reaction mixture with a PM1 forward primer and a PM1 reverse primer, wherein the PM1 forward primer and the PM1 reverse primer bind to sites nested within the amplified portion of the *AHAS1* gene;

e) denaturing the product of the second amplification step to produce single stranded polynucleotides that are allowed to adopt unique conformations by intramolecular interactions; and

f) detecting the presence or absence of the PM1 mutation on the basis of the mobility of said single stranded polynucleotide conformers in a substrate.

4 (currently amended). The method of claim ~~1~~ 2 or 3, wherein the PM1 forward primer has a sequence as set forth in nucleotides 1 to 21 of SEQ ID NO:11.

5 (currently amended). The method of claim ~~1~~ 2 or 3, wherein the PM1 reverse primer has a sequence as set forth in nucleotides 1 to 21 of SEQ ID NO:12.

6 (currently amended). The method of claim ~~1~~ 2 or 3, wherein step ~~e~~ (d) includes incorporating a label into the amplified portion of the *AHAS1* gene.

7. The method of claim 6, wherein the label is selected from the group consisting of a radioactive label, a fluorescent label, a luminescent label, and a paramagmetic label.

8 (currently amended). The method of claim ~~1~~ 2 or 3, wherein the substrate is selected from the group consisting of polyacrylamide, linear polyacrylamide, poly(N,N-dimethylacrylamide), hydroxyalkyl cellulose, polyoxyethylene, F127, agarose, diethylaminoethyl cellulose, sepharose, POP4, and POP6.

9 (currently amended). The method of claim ~~1~~ 2 or 3, wherein the detection method is selected from the group consisting of electrophoresis and chromatography.

10 (currently amended). The method of claim ~~1~~ 2 or 3, further comprising the step of detecting the presence or absence of PM2-mediated imidazolinone resistance in the plant.

11 (canceled).

12 (currently amended). ~~The~~ A method ~~of claim 11, wherein wherein the~~ for assaying a *Brassica* plant for imidazolinone herbicide tolerance conferred by the PM2 mutation of the *B. napus AHAS3* gene, the method comprising the steps of:

a) isolating genomic DNA from the plant;

b) selectively amplifying the *AHAS3* gene from the genomic DNA using an *AHAS3* forward primer ~~has the~~ having a sequence as set forth in nucleotides 1 to 22 of SEQ ID NO:13 and an *AHAS3* reverse primer in a first amplification step to produce an *AHAS3* reaction mixture;

c) removing the *AHAS3* primers from the *AHAS3* reaction mixture to produce a purified *AHAS3* reaction mixture;

d) in a second amplification step, further amplifying the amplified *AHAS3* gene, by combining a first aliquot of the purified *AHAS3* reaction mixture with a PM2 region forward primer, a PM2 region reverse primer, and a primer selective for a wild type allele of the PM2 region at position 1712 of the *AHAS3* gene as depicted in SEQ ID NOs:5 and 8;

e) in a third amplification step further amplifying the amplified *AHAS3* gene, by combining a second aliquot of the purified *AHAS3* reaction mixture with a PM2 region forward primer, a PM2 region reverse primer, and a primer selective for the PM2 mutation; and

f) analyzing the amplified first and second aliquots for the presence or absence of the PM2 mutation.

13 (currently amended). ~~The~~ A method ~~of claim 11, wherein the~~ for assaying a *Brassica* plant for imidazolinone herbicide tolerance conferred by the PM2 mutation of the *B. napus AHAS3* gene, the method comprising the steps of:

a) isolating genomic DNA from the plant;

b) selectively amplifying the *AHAS3* gene from the genomic DNA using an *AHAS3* forward primer and an *AHAS3* reverse primer ~~has the~~ having a sequence as set forth in nucleotides 1 to 23 of SEQ ID NO:14 in a first amplification step to produce an *AHAS3* reaction mixture;

c) removing the *AHAS3* primers from the *AHAS3* reaction mixture to produce a purified *AHAS3* reaction mixture;

d) in a second amplification step, further amplifying the amplified *AHAS3* gene, by combining a first aliquot of the purified *AHAS3* reaction mixture with a PM2 region forward primer, a PM2 region reverse primer, and a primer selective for a wild type allele of the PM2 region at position 1712 of the *AHAS3* gene as depicted in SEQ ID NOs:5 and 8;

e) in a third amplification step further amplifying the amplified *AHAS3* gene, by combining a second aliquot of the purified *AHAS3* reaction mixture with a PM2 region forward primer, a PM2 region reverse primer, and a primer selective for the PM2 mutation; and

f) analyzing the amplified first and second aliquots for the presence or absence of the PM2 mutation.

14 (currently amended). The method of claim ~~11~~ 12 or 13, wherein the PM2 region forward primer has a sequence as set forth in nucleotides 1 to 19 of SEQ ID NO:15.

15 (currently amended). The method of claim ~~11~~ 12 or 13, wherein the PM2 region reverse primer has a sequence as set forth in nucleotides 1 to 19 of SEQ ID NO:16.

16 (currently amended). The method of claim ~~11~~ 12 or 13, wherein the wild type allele of the PM2 region at position 1712 has a sequence as set forth in nucleotides 1 to 18 of SEQ ID NO:17.

17 (currently amended). The method of claim ~~11~~ 12 or 13, wherein the primer selective for the PM2 mutation has a sequence as set forth in nucleotides 1 to 20 of SEQ ID NO:18.

18 (currently amended). The method of claim ~~11~~ 12 or 13, wherein steps ~~e~~ (d) and ~~d~~ (e) include incorporating a label into the amplified portion of the *AHAS3* gene.

19. The method of claim 18, wherein the label is selected from the group consisting of a radioactive label, a fluorescent label, a luminescent label, and a paramagmetic label.

20 (currently amended). The method of claim ~~11~~ 12 or 13, wherein the analyzing step employs a method selected from the group consisting of electrophoresis and chromatography.

21 (currently amended). The method of claim ~~11~~ 12 or 13, further comprising the steps of:

g) selectively amplifying an *AHAS1* gene from the genomic DNA using an *AHAS1* forward primer and an *AHAS1* reverse primer in a fourth amplification step;

h) removing the *AHAS1* primers from the product of step g);

i) in a fifth amplification step, further amplifying a portion of the amplified *AHAS1* gene containing the site of the PM1 mutation, by combining the product of step h) with a PM1 forward primer and a PM1 reverse primer, wherein the PM1 forward primer and the PM1 reverse primer ~~are~~ bind to sites nested within the amplified portion of the *AHAS1* ~~forward and reverse primers~~ gene;

j) denaturing the product of the fifth amplification step to produce single stranded polynucleotides that are allowed to adopt unique conformations by intramolecular interactions; and

k) detecting the presence or absence of the PM1 mutation on the basis of the mobility of said single stranded conformer polynucleotides in a substrate.

22. (canceled).

23. (canceled).

24 (currently amended). A method of marker assisted breeding of plants of *Brassica* species using a PM1 mutation of the *B. napus AHAS1* gene as a marker, the method comprising the steps of:

a) isolating genomic DNA from a *Brassica* plant;

b) selectively amplifying an *AHAS1* gene from the genomic DNA using an *AHAS1* forward primer having a sequence as set forth in nucleotides 1

to 22 of SEQ ID NO:9 and an *AHAS1* reverse primer in a first amplification step, thereby producing an *AHAS1* reaction mixture;

c) removing the *AHAS1* primers from the *AHAS1* reaction mixture to produce a purified *AHAS1* reaction mixture;

d) in a second amplification step, further amplifying a portion of the amplified *AHAS1* gene containing the site of the PM1 mutation, by combining the purified *AHAS1* reaction mixture with a PM1 forward primer and a PM1 reverse primer, wherein the PM1 forward primer and the PM1 reverse primer ~~are~~ bind to sites nested within the amplified portion of the *AHAS1* ~~forward and reverse primers~~ gene;

e) denaturing the product of the second amplification step to produce single stranded polynucleotides that are allowed to adopt unique conformations by intramolecular interactions;

f) detecting the presence or absence of the PM1 mutation on the basis of the mobility of said single stranded polynucleotide conformers in a substrate: and

g) selecting said plant as a parent for further breeding if the PM1 mutation is present.

25. A method of marker assisted breeding of plants of *Brassica* species using a PM2 mutation of the *B. napus AHAS3* gene as a marker, the method comprising the steps of:

a) isolating genomic DNA from the plant;

b) selectively amplifying the *AHAS3* gene from the genomic DNA using an *AHAS3* forward primer and an *AHAS3* reverse primer having a sequence as set forth in nucleotides 1 to 22 of SEQ ID NO:10 in a first amplification step to produce an *AHAS3* reaction mixture;

c) removing the *AHAS3* primers from the *AHAS3* reaction mixture to produce a purified *AHAS3* reaction mixture;

d) in a second amplification step, further amplifying the amplified *AHAS3* gene, by combining a first aliquot of the purified *AHAS3*

reaction mixture with a PM2 region forward primer, a PM2 region reverse primer, and a primer selective for a wild type allele of the PM2 region at position 1712 of the *AHAS3* gene as depicted in SEQ ID NOs:5 and 8;

e) in a third amplification step further amplifying the amplified *AHAS3* gene, by combining a second aliquot of the purified *AHAS3* reaction mixture with a PM2 region forward primer, a PM2 region reverse primer, and a primer selective for the PM2 mutation;

f) analyzing the amplified first and second aliquots for the presence or absence of the PM2 mutation; and

g) selecting said plant as a parent for further breeding if the PM2 mutation is present.